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Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

> alignment of SEQ ID NO:4 and 17

Sequence 1: UserSeq4, (654 residues)
Sequence 2: UserSeq17, (1246 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4

Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

```
100.0% identity in 654 residues overlap; Score: 3446.0; Gap frequency: 0.0%

UserSeq4,      1 QVLKGRMDSEQSPSIGYSSRTLGPNPGLILQALTLSNASDGFNLERLEMLGDSFLKHAIT
UserSeq17,   593 QVLKGRMDSEQSPSIGYSSRTLGPNPGLILQALTLSNASDGFNLERLEMLGDSFLKHAIT
                 ************************************************************

UserSeq4,     61 TYLFCTYPDAHEGRLSYMRSKKVSNCNLYRLGKKKGLPSRMVVSIFDPPVNWLPPGYVVN
UserSeq17,   653 TYLFCTYPDAHEGRLSYMRSKKVSNCNLYRLGKKKGLPSRMVVSIFDPPVNWLPPGYVVN
                 ************************************************************

UserSeq4,    121 QDKSNTDKWEKDEMTKDCMLANGKLDEDYEEEDEEEESLMWRAPKEEADYEDDFLEYDQE
UserSeq17,   713 QDKSNTDKWEKDEMTKDCMLANGKLDEDYEEEDEEEESLMWRAPKEEADYEDDFLEYDQE
                 ************************************************************

UserSeq4,    181 HIRFIDNMLMGSGAFVKKISLSPFSTTDSAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDA
UserSeq17,   773 HIRFIDNMLMGSGAFVKKISLSPFSTTDSAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDA
                 ************************************************************
```

```
UserSeq4,    241 MCYLDPSKAVEEDDFVVGFWNPSEENCGVDTGKQSISYDLHTEQCIADKSIADCVEALLG
UserSeq17,   833 MCYLDPSKAVEEDDFVVGFWNPSEENCGVDTGKQSISYDLHTEQCIADKSIADCVEALLG
                 ************************************************************


UserSeq4,    301 CYLTSCGERAAQLFLCSLGLKVLPVIKRTDREKALCPTRENFNSQQKNLSVSCAAASVAS
UserSeq17,   893 CYLTSCGERAAQLFLCSLGLKVLPVIKRTDREKALCPTRENFNSQQKNLSVSCAAASVAS
                 ************************************************************


UserSeq4,    361 SRSSVLKDSEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKINYRFKNKAYLLQAFT
UserSeq17,   953 SRSSVLKDSEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKINYRFKNKAYLLQAFT
                 ************************************************************


UserSeq4,    421 HASYHYNTITDCYQRLEFLGDAILDYLITKHLYEDPRQHSPGVLTDLRSALVNNTIFASL
UserSeq17,  1013 HASYHYNTITDCYQRLEFLGDAILDYLITKHLYEDPRQHSPGVLTDLRSALVNNTIFASL
                 ************************************************************


UserSeq4,    481 AVKYDYHKYFKAVSPELFHVIDDFVQFQLEKNEMQGMDSELRRSEEDEEKEEDIEVPKAM
UserSeq17,  1073 AVKYDYHKYFKAVSPELFHVIDDFVQFQLEKNEMQGMDSELRRSEEDEEKEEDIEVPKAM
                 ************************************************************


UserSeq4,    541 GDIFESLAGAIYMDSGMSLETVWQVYYPMMRPLIEKFSANVPRSPVRELLEMEPETAKFS
UserSeq17,  1133 GDIFESLAGAIYMDSGMSLETVWQVYYPMMRPLIEKFSANVPRSPVRELLEMEPETAKFS
                 ************************************************************


UserSeq4,    601 PAERTYDGKVRVTVEVVGKGKFKGVGRSYRIAKSAAARRALRSLKANQPQVPNS
UserSeq17,  1193 PAERTYDGKVRVTVEVVGKGKFKGVGRSYRIAKSAAARRALRSLKANQPQVPNS
                 *****************************************************
```

39.0% identity in 41 residues overlap; Score: 64.0; Gap frequency: 0.0%

```
UserSeq4,    434 QRLEFLGDAILDYLITKHLYEDPRQHSPGVLTDLRSALVNN
UserSeq17,   637 ERLEMLGDSFLKHAITTYLFCTYPDAHEGRLSYMRSKKVSN
                 *** ***   *   **  *       * *   **   * *
```

39.0% identity in 41 residues overlap; Score: 64.0; Gap frequency: 0.0%

```
UserSeq4,     45 ERLEMLGDSFLKHAITTYLFCTYPDAHEGRLSYMRSKKVSN
UserSeq17,  1026 QRLEFLGDAILDYLITKHLYEDPRQHSPGVLTDLRSALVNN
                 *** ***   *   **  *              * *   **  * *
```

28.8% identity in 52 residues overlap; Score: 50.0; Gap frequency: 0.0%

```
UserSeq4,    124 SNTDKWEKDEMTKDCMLANGKLDEDYEEEDEEEESLMWRAPKEEADYEDDFL
UserSeq17,   797 STTDSAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDAMCYLDPSKAVEEDDFV
                 *  **     *  *   *     * *  *        *       *  ****
```

28.8% identity in 52 residues overlap; Score: 50.0; Gap frequency: 0.0%

```
UserSeq4,    205 STTDSAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDAMCYLDPSKAVEEDDFV
UserSeq17,   716 SNTDKWEKDEMTKDCMLANGKLDEDYEEEDEEEESLMWRAPKEEADYEDDFL
```